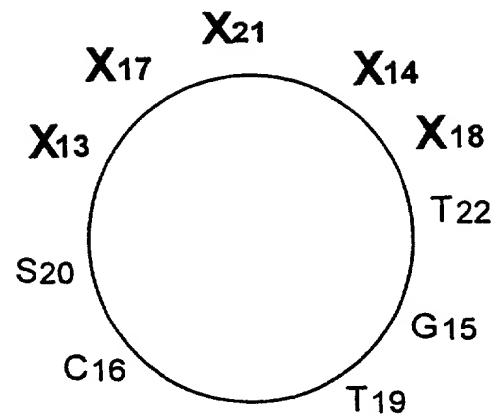
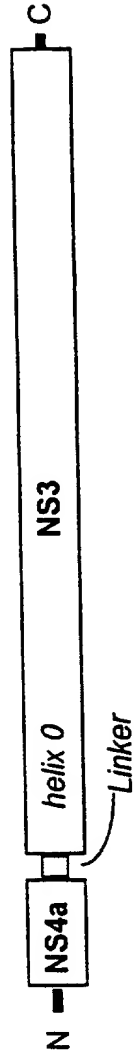
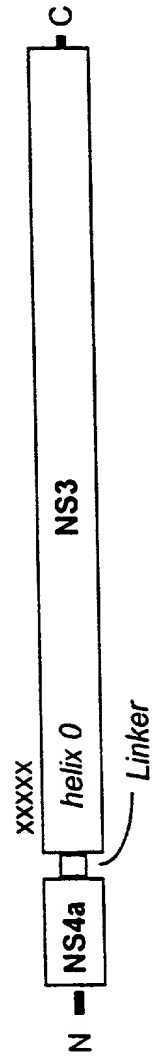


[illegible]

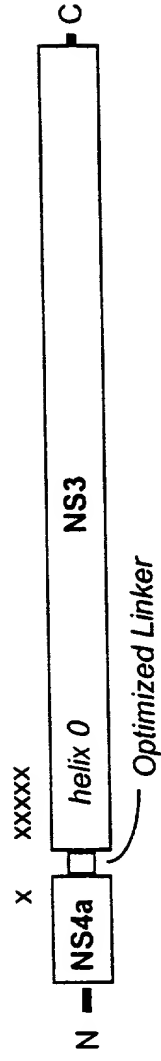
SEQ ID NO:3



SEQ ID NO:5,



SEQ ID NO:14



SEQ ID NO:18

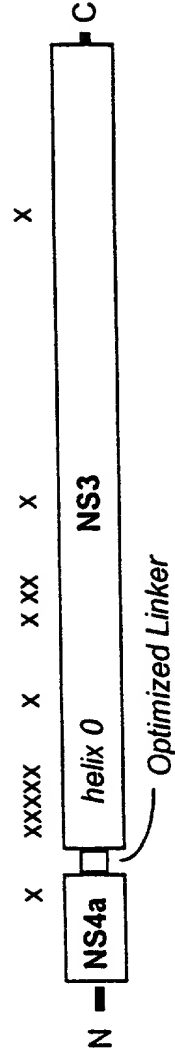


FIG. 2

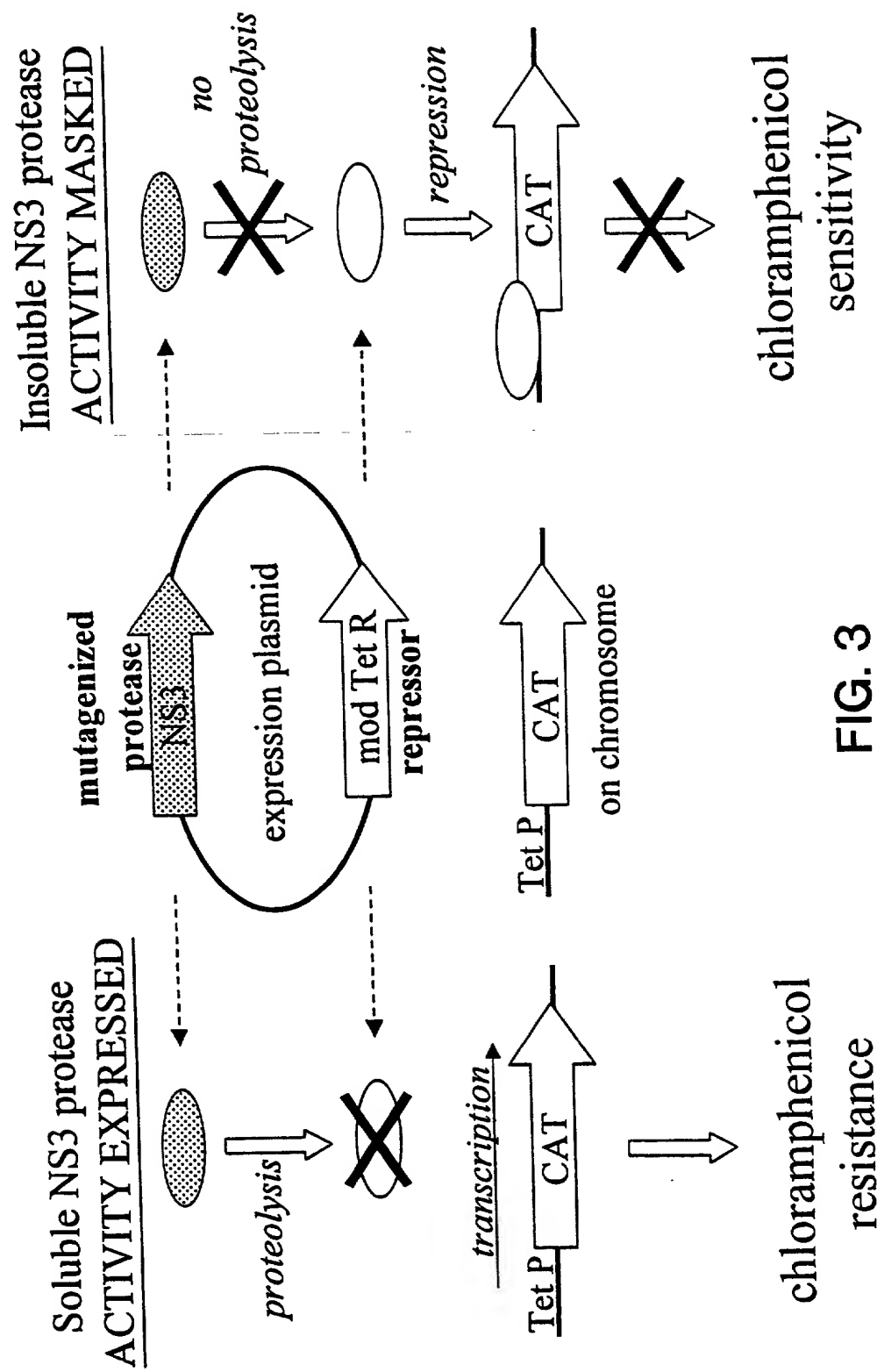


FIG. 3

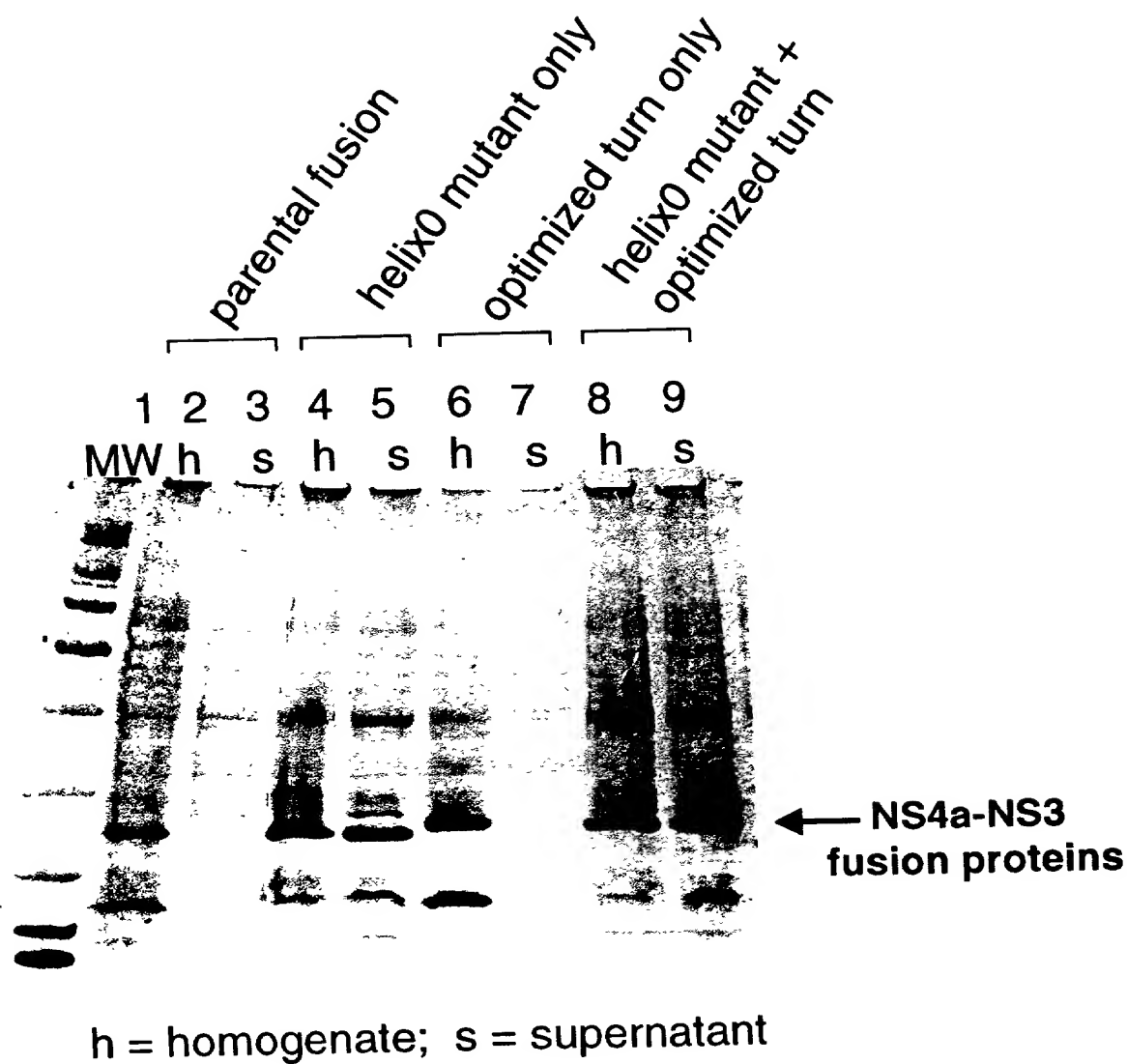


FIG. 4

SEQ ID NO:5

HN

N

100.0

110.0

120.0

130.0

10.0

8.0

6.0

FIG. 5A

SEQ ID NO:14

N

100.0

110.0

120.0

130.0

10.0

8.0

6.0

HN

FIG. 5B

FIG. 5B

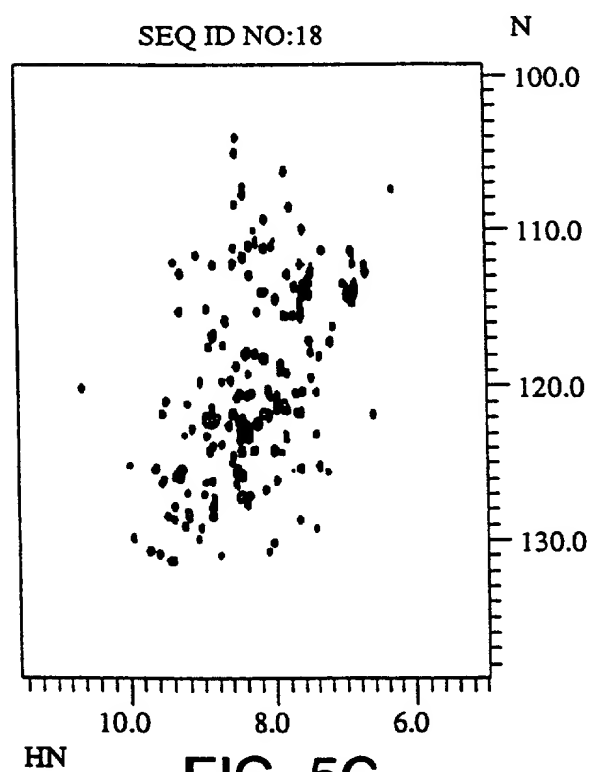


FIG. 5C

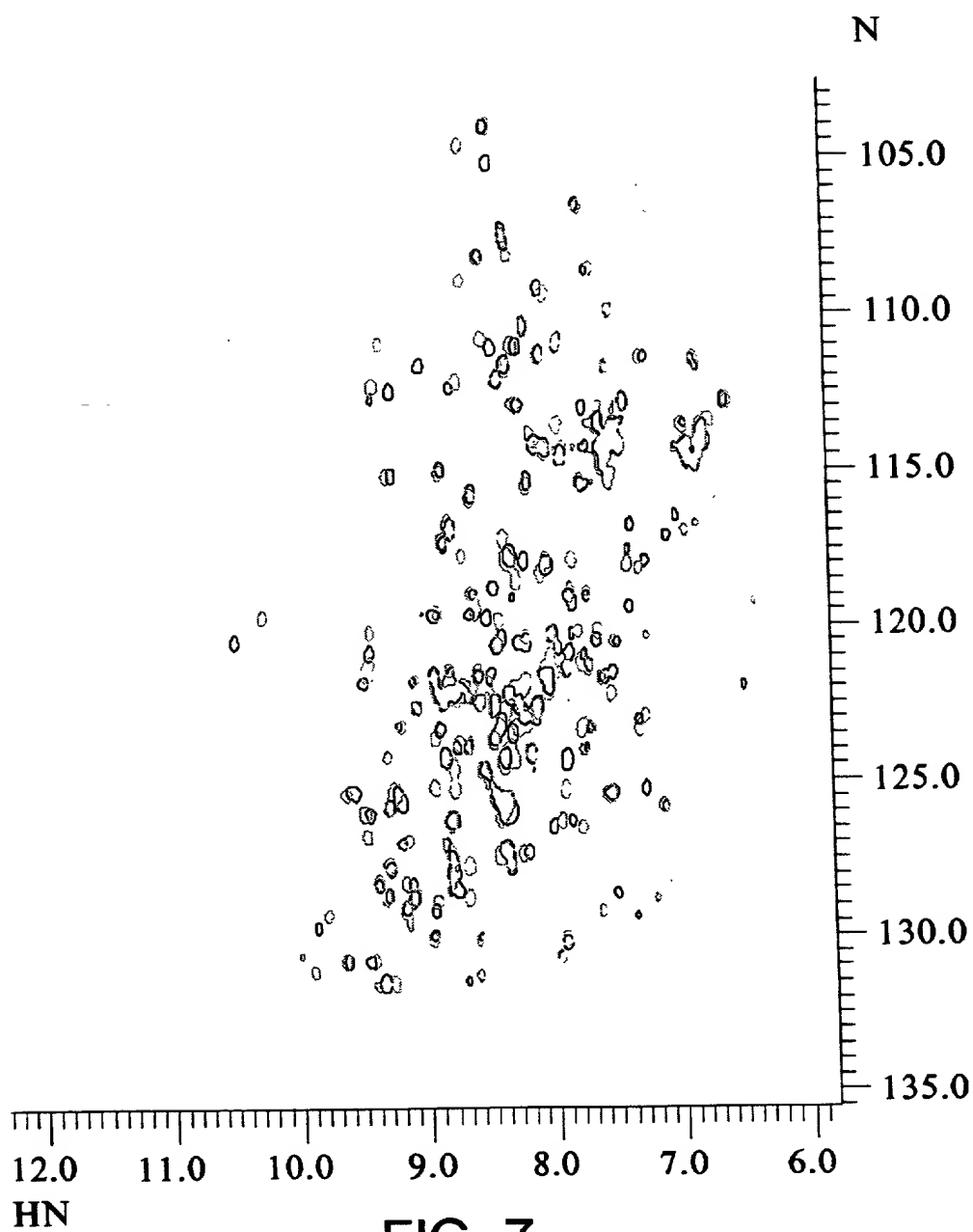
Seq ID NO:1	1	2	3	4	5	6
Seq ID NO:3	5	0	0	0	0	0
Seq ID NO:12	-----MAPITAYAAQOTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVWTVYHGAGTRTIA					
Seq ID NO:14	MKKKGSVWIVGRIVL-NG-AYAQQOTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVWTVYHGAGTRTIA					
Seq ID NO:16	MKKKGSVWIVGRIVL-NG-AYAQQOTRGECCQETSQTGRDKNQVEGEVQIVSTAAQTFLATCINGVWTVYHGAGTRTIA					
Seq ID NO:18	MKKKGSVWIVGRINI-NG-AYAQQOTRGECCQETSQTGRDKNQVEGEVQIVSTAAQTFLATCINGVWTVYHGAGTRTIA					
Seq ID NO:20	MKKKGSVWIVGRINI-NG-AYAQQOTRGECCQETSQTGRDKNQVEGEVQIVSTAAQTFLATCINGVWTVYHGAGTRTIA					
Seq ID NO:22	MKKKGSVWIVGRINI-NG-AYAQQOTRGECCQETSQTGRDKNQVEGEVQIVSTAAQTFLATCINGVWTVYHGAGTRTIA					
Seq ID NO:24	MKKKGSVWIVGRINI-NG-AYAQQOTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVWTVYHGAGTRTIA					

Seq ID NO:1	1	1	1	1	1	1
Seq ID NO:3	7	8	9	0	1	4
Seq ID NO:12	0	0	0	0	3	0
Seq ID NO:14	SPKGPVIQMYTNVVDKDLVGPAPQGGSRSLTPCTCGSSDLYLVTRHADVI PVRRRGDSRGSLLSPRPISYLVKSSGGPLLC					
Seq ID NO:16	SPKGPVIQMYTNVVDKDLVGPAPQGGSRSLTPCTCGSSDLYLVTRHADVI PVRRRGDSRGSLLSPRPISYLVKSSGGPLLC					
Seq ID NO:18	SPKGPVIQMYTNVVDKDLVGPAPQGGSRSLTPCTCGSSDLYLVTRHADVI PVRRRGDSRGSLLSPRPISYLVKSSGGPLLC					
Seq ID NO:20	SPKGPVIQMYTNVVDKDLVGPAPQGGSRSLTPCTCGSSDLYLVTRHADVI PVRRRGDSRGSLLSPRPISYLVKSSGGPLLC					
Seq ID NO:22	SPKGPVIQMYTNVVDKDLVGPAPQGGSRSLTPCTCGSSDLYLVTRHADVI PVRRRGDSRGSLLSPRPISYLVKSSGGPLLC					
Seq ID NO:24	SPKGPVIQMYTNVVDKDLVGPAPQGGSRSLTPCTCGSSDLYLVTRHADVI PVRRRGDSRGSLLSPRPISYLVKSSGGPLLC					

Seq ID NO:1	1	1	1	1	1	1
Seq ID NO:3	5	6	7	8	8	8
Seq ID NO:12	0	0	0	0	0	0
Seq ID NO:14	PAGHAVGIFRAAVCTRGVAKAVDFIPVESLETMRSP--					
Seq ID NO:16	PAGHAVGIFRAAVCTRGVAKAVDFIPVESLETMRSP--					
Seq ID NO:18	PAGHAVGIFRAAVCTRGVAKAVDFIPVESLETMRSP--					
Seq ID NO:20	PAGHAVGIFRAAVCTRGVAKAVDFIPVESLETMRSP--					
Seq ID NO:22	PAGHAVGIFRAAVCTRGVAKAVDFIPVESLETMRSP--					
Seq ID NO:24	PAGHAVGIFRAAVCTRGVAKAVDFIPVESLETMRSP--					

FIG. 6

60260 465560



A complex, multi-lobed wireframe structure, possibly representing a molecular model or a mathematical surface, rendered in black lines on a white background. The structure consists of several interconnected, irregularly shaped volumes. Each volume is defined by a dense network of intersecting lines, creating a mesh-like appearance. The overall shape is elongated and somewhat symmetrical, with a central region where the different lobes meet. The lines are thin and black, providing a clear outline of the structure's geometry.

 1.00 A

M A P I T A Y A Q Q T R G L L G C I I T
 1 ATGGCTCCGAT CACCGCTTA CGCTCAGCAG ACCCGTGGTC TGCTGGGTTG CATCATCACC
 TACCGAGGCT AGTGGCGAAT GCGAGTCGTC TGGGCACCAG ACGACCCAAC GTAGTAGTGG

 S L T G R D K N Q V E G E V Q I V S T A
 61 TCCCTGACCG GTCGTGACAA AAACCAGGTT GAAGGTGAAG TTCAGATCGT TTCCACCGCT
 AGGGACTGGC CAGCACTGTT TTTGGTCCAA CTTCCACTTC AAGTCTAGCA AAGGTGGCGA

 A Q T F L A T C I N G V C W T V Y H G A
 121 GCTCAGACCT TCCTGGCTAC CTGCATCAAC GGTGTTTGCT GGACCGTTTA CCACGGTGCT
 CGAGTCTGGA AGGACCGATG GACGTAGTTG CCACAAACGA CCTGGCAAAT GGTGCCACGA

 G T R T I A S P K G P V I Q M Y T N V D
 181 GGTACCCGTA CCATCGCTTC CCCGAAAGGT CCGGTTATCC AGATGTACAC CAACGTTGAC
 CCATGGGCAT GGTAGCGAAG GGGCTTTCCA GGCCAATAGG TCTACATGTG GTTGCAACTG

 K D L V G W P A P Q G S R S L T P C T C
 241 AAAGACCTGG TTGGTTGGCC GGCTCCGCAG GGTTCCTCGTT CCCTGACCCC GTGCACCTGC
 TTTCTGGACC AACCAACCGG CCGAGGCGTC CCAAGGGCAA GGGACTGGGG CACGTGGACG

 G S S D L Y L V T R H A D V I P V R R R
 301 GGTTCCTCCG ACCTGTACCT GGTACCCGT CACGCTGACG TTATCCCGGT TCGTCGTCGT
 CCAAGGAGGC TGGACATGGA CCAATGGGCA GTGCGACTGC AATAGGGCCA AGCAGCAGCA

 G D S R G S L L S P R P I S Y L K G S S
 361 GGTGACTCCC GTGGTTCCCT GCTGTCCCCG CGTCCGATCT CCTACCTGAA AGGTTCCCTCC
 CCACTGAGGG CACCAAGGGA CGACAGGGGC GCAGGCTAGA GGATGGACTT TCCAAGGAGG

 G G P L L C P A G H A V G I F R A A V C
 421 GGTGGTCCGC TGCTGTGCCC GGCTGGTCAC GCTGTTGGTA TCTTCCGTGC TGCTGTTTGC
 CCACCAGGCG ACGACACGGG CCGACCAGTG CGACAACCAT AGAAGGCACG ACGACAAACG

 T R G V A K A V D F I P V E S L E T T M
 481 ACCCGTGGTG TTGCTAAAGC TGTTGACTTC ATCCCGGTTG AATCCCTGGA AACCACCATG
 TGGGCACCAC AACGATTTTC ACAACTGAAG TAGGGCCAAC TTAGGGACCT TTGGTGGTAC

 R S *
 541 CGTTCCTGA
 GCAAGGACT

FIG. 9

M K K K G S V V I V G R I V L N G A Y A
1 ATGAAAAAAAA AAGGTTCCGT TGTATCGTC GGCCGTATAG TACTGAACGG TGCTTACGCT
TACTTTTTTT TTCCAAGGCA ACAATAGCAG CCGGCATATC ATGACTTGCC ACGAATGCGA

Q Q T R G L L G C I I T S L T G R D K N
61 CAGCAGACTC GAGGTCTGCT GGGTTGCATC ATCACCTCCC TGACCGGTCG TGACAAAAAC
GTCGTCTGAG CTCCAGACGA CCCAACGTAG TAGTGGAGGG ACTGGCCAGC ACTGTTTTTG

Q V E G E V Q I V S T A A Q T F L A T C
121 CAGGTTGAAG GTGAAGTTCA GATCGTTTCC ACCGCTGCTC AGACCTTCCT GGCTACCTGC
GTCCAACCTC CACTTCAAGT CTAGCAAAGG TGGCGACGAG TCTGGAAGGA CCGATGGACG

I N G V C W T V Y H G A G T R T I A S P
181 ATCAACGGTG TTTGCTGGAC CGTTTACCAC GGTGCTGGTA CCCGTACCAT CGCTTCCCCG
TAGTTGCCAC AAACGACCTG GCAAATGGTG CCACGACCAT GGGCATGGTA GCGAAGGGGC

K G P V I Q M Y T N V D K D L V G W P A
241 AAAGGTCCGG TTATCCAGAT GTACACCAAC GTTGACAAAG ACCTGGTTGG TTGGCCGGCT
TTTCCAGGCC AATAGGTCTA CATGTGGTTG CAACTGTTTC TGGACCAACC AACC GGCCGA

P Q G S R S L T P C T C G S S D L Y L V
301 CCGCAGGGTT CCCGTTCCCT GACCCCGTGC ACCTGCGGTT CCTCCGACCT GTACCTGGTT
GGCGTCCCAA GGGCAAGGGA CTGGGGGCACG TGGACGCCAA GGAGGCTGGA CATGGACCAA

T R H A D V I P V R R R G D S R G S L L
361 ACCCGTCACG CTGACGTTAT CCCGGTTTCGT CGTCGTGGTG ACTCCCGTGG TTCCCTGCTG
TGGGCAGTGC GACTGCAATA GGGCCAAGCA GCAGCACCAC TGAGGGCACC AAGGGACGAC

S P R P I S Y L K G S S G G P L L C P A
421 TCCCCGCGTC CGATCTCCTA CCTGAAAGGT TCCTCCGGTG GTCCGCTGCT GTGCCCCGGCT
AGGGGCGCAG GCTAGAGGAT GGACTTTCCA AGGAGGCCAC CAGGCGACGA CACGGGCCGA

G H A V G I F R A A V C T R G V A K A V
481 GGTCACGCTG TTGGTATCTT CCGTGCTGCT GTTTGCACCC GTGGTGTGTC TAAAGCTGTT
CCAGTGCGAC AACCATAGAA GGCACGACGA CAAACGTGGG CACCACAACG ATTTGACAA

D F I P V E S L E T T M R S P *
541 GACTTCATCC CGGTTGAATC CCTGGAAACC ACCATGCGTT CCCCCTGA
CTGAAGTAGG GCCAACTTAG GGACCTTTGG TGGTACGCAA GGGGCACT

FIG. 10

						L ₁₃	L ₁₄			I ₁₇	I ₁₈			L ₂₁		
Wild-type	(5)	Q	Q	T	R	G	L	L	G	C	I	I	T	S	L	T
Helix0-1	(6)	E	E	.	.	Q	E	.	.	Q	.
Helix0-3	(7)	E	E	.	.	Q	Q	.	.	E	.
Helix0-4	(8)	N	Q	.	.	E	K	.	.	E	.
Helix0-7	(9)	E	Q	.	.	Q	K	.	.	H	.
Helix0-8	(10)	E	Q	.	.	D	E	.	.	E	.
Helix0-10	(11)	E	E	.	.	E	Q	.	.	E	.

FIG. 11

M K K K G S V V I V G R I V L N G A Y A
 1 ATGAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATAG TACTGAACGG TGCTTACGCT
 TACTTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATATC ATGACTTGCC ACGAATGCGA

 Q Q T R G E E G C Q E T S Q T G R D K N
 61 CAGCAGACTC GAGGTGAGGA GGGTTGCCAA GAAACCTCCC AGACCGGTCG TGACAAAAAC
 GTCGTCTGAG CTCCACTCCT CCCAACGGTT CTTTGGAGGG TCTGGCCAGC ACTGTTTTTG

 Q V E G E V Q I V S T A A Q T F L A T C
 121 CAGGTTGAAG GTGAAGTTCA GATCGTTTCC ACCGCTGCTC AGACCTTCCT GGCTACCTGC
 GTCCAACTTC CACTTCAAGT CTAGCAAAGG TGGCGACGAG TCTGGAAGGA CCGATGGACG

 I N G V C W T V Y H G A G T R T I A S P
 181 ATCAACGGTG TTTGCTGGAC CGTTTACCAC GGTGCTGGTA CCCGTACCAT CGCTTCCCCG
 TAGTTGCCAC AAACGACCTG GCAAATGGTG CCACGACCAT GGGCATGGTA GCGAAGGGGG

 K G P V I Q M Y T N V D K D L V G W P A
 241 AAAGGTCCGG TTATCCAGAT GTACACCAAC GTTGACAAAG ACCTGGTTGG TTGGCCGGCT
 TTTCCAGGCC AATAGGTCTA CATGTGGTTG CAACTGTTTC TGGACCAACC AACC GGCCGA

 P Q G S R S L T P C T C G S S D L Y L V
 301 CCGCAGGGTT CCCGTTCCCT GACCCCGTGC ACCTGCGGTT CCTCCGACCT GTACCTGGTT
 GGCGTCCCAA GGGCAAGGGA CTGGGGCAGC TGGACGCCAA GGAGGCTGGA CATGGACCAA

 T R H A D V I P V R R R G D S R G S L L
 361 ACCCGTCACG CTGACGTTAT CCCGGTTTCG CGTCGTGGTG ACTCCCGTGG TTCCCTGCTG
 TGGGCAGTGC GACTGCAATA GGGCCAAGCA GCAGCACCAC TGAGGGCACC AAGGGACGAC

 S P R P I S Y L K G S S G G P L L C P A
 421 TCCCCGCGTC CGATCTCCTA CCTGAAAGGT TCCTCCGGTG GTCCGCTGCT GTGCCCGGCT
 AGGGGCGCAG GCTAGAGGAT GGACTTTCCA AGGAGGCCAC CAGGCGACGA CACGGGCCGA

 G H A V G I F R A A V C T R G V A K A V
 481 GGTCACGCTG TTGGTATCTT CCGTGCTGCT GTTTGCACCC GTGGTGTTCG TAAAGCTGTT
 CCAGTGCGAC AACCATAGAA GGCACGACGA CAAACGTGGG CACCACAACG ATTTGACAA

 D F I P V E S L E T T M R S P *
 541 GACTTCATCC CGGTTGAATC CCTGGAAACC ACCATGCGTT CCCCCTGA
 CTGAAGTAGG GCCAAGTTAG GGACCTTTGG TGGTACGCAA GGGGCACT

FIG. 12

M K K K G S V V I V G R I N L S G D T A
 1 ATGAAAAAAA AAGGATCCGT TGTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT
 TACTTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA

 Y A Q Q T R G E E G C Q E T S Q T G R D
 61 TACGCTCAGC AGACTCGAGG TGAGGAGGGT TGCCAAGAAA CCTCCCAGAC CGGTCGTGAC
 ATGCGAGTCG TCTGAGCTCC ACTCCTCCCA ACGGTTCTTT GGAGGGTCTG GCCAGCACTG

 K N Q V E G E V Q I V S T A A Q T F L A
 121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCACCG CTGCTCAGAC CTTCTGGCT
 TTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GACGAGTCTG GAAGGACCGA

 T C I N G V C W T V Y H G A G T R T I A
 181 ACCTGCATCA ACGGTGTTTG CTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT
 TGGACGTAGT TGCCACAAAC GACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA

 S P K G P V I Q M Y T N V D K D L V G W
 241 TCCCCGAAAG GTCCGGTTAT CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTTGGTTGG
 AGGGGCTTTC CAGGCCAATA GGTCTACATG TGTTTGAAC TGTTTCTGGA CCAACCAACC

 P A P Q G S R S L T P C T C G S S D L Y
 301 CCGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGACCT GCGGTTCCCTC CGACCTGTAC
 GGCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG

 L V T R H A D V I P V R R R G D S R G S
 361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGACTC CCGTGGTTCC
 GACCAATGGG CAGTGC GACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG

 L L S P R P I S Y L K G S S G G P L L C
 421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTCTT CCGGTGGTCC GCTGCTGTGC
 GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACACG

 P A G H A V G I F R A A V C T R G V A K
 481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT GCACCCGTGG TGTGCTAAA
 GGCCGACCAG TGCGACAACC ATAGAAGGCA CGACGACAAA CGTGGGCACC ACAACGATTT

 A V D F I P V E S L E T T M R S P *
 541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGC GTTCCCC GTGA
 CGACA ACTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

FIG. 13

M K K K G S V V I V G R I N L S G D T A
 1 ATGAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT
 TACTTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA

 Y A Q Q T R G E E G C Q E T S Q T G R D
 61 TACGCTCAGC AGACTCGAGG TGAGGAGGGT TGCCAAGAAA CCTCCCAGAC CGGTCGTGAC
 ATGCGAGTCG TCTGAGCTCC ACTCCTCCCA ACGGTTCTTT GGAGGGTCTG GCCAGCACTG

 K N Q V E G E V Q I V S T A T Q T F L A
 121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCACCG CTACCCAGAC CTTCTGGCT
 TTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GATGGGTCTG GAAGGACCGA

 T C I N G V C W T V Y H G A G T R T I A
 181 ACCTGCATCA ACGGTGTTTG CTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT
 TGGACGTAGT TGCCACAAAC GACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA

 S P K G P V T Q M Y T N V D K D L V G W
 241 TCCCCGAAAG GTCCGGTTAC CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTGTTGGTGG
 AGGGGCTTTC CAGGCCAATG GGTCTACATG TGGTTGCAAC TGTTTCTGGA CCAACCAACC

 Q A P Q G S R S L T P C T C G S S D L Y
 301 CAGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGACCT GCGGTTCCCTC CGACCTGTAC
 GTCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG

 L V T R H A D V I P V R R R G D S R G S
 361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGACTC CCGTGGTTCC
 GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG

 L L S P R P I S Y L K G S S G G P L L C
 421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTCTT CCGGTGGTCC GCTGCTGTGC
 GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACACG

 P A G H A V G I F R A A V C T R G V A K
 481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT GCACCCGTGG TGTGCTAAA
 GGCCGACCAG TGCGACAACC ATAGAAGGCA CGACGACAAA CGTGGGCACC ACAACGATTT

 A V D F I P V E S L E T T M R S P *
 541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGCGTTCCCC GTGA
 CGACAACCTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

FIG. 14

M K K K G S V V I V G R I N L S G D T A
 1 ATGAAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT
 TACTTTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA

 Y A Q Q T R G E E G C Q E T S Q T G R D
 61 TACGCTCAGC AGACTCGAGG TGAGGAGGGT TGCCAAGAAA CCTCCCAGAC CGGTTCGTGAC
 ATGCGAGTCG TCTGAGCTCC ACTCCTCCCA ACGGTTCTTT GGAGGGTCTG GCCAGCACTG

 K N Q V E G E V Q I V S T A T Q T F L A
 121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCCACCG CTACCCAGAC CTTCTCGGCT
 TTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GATGGGTCTG GAAGGACCGA

 T S I N G V L W T V Y H G A G T R T I A
 181 ACCTCCATCA ACGGTGTTCT GTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT
 TGGAGGTAGT TGCCACAAGA CACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA

 S P K G P V T Q M Y T N V D K D L V G W
 241 TCCCCGAAAG GTCCGGTTAC CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTGTTGGTGG
 AGGGGCTTTC CAGGCCAATG GGTCTACATG TGGTTGCAAC TGTTTCTGGA CCAACCAACC

 Q A P Q G S R S L T P C T C G S S D L Y
 301 CAGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGCACCT GCGGTTCCCTC CGACCTGTAC
 GTCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG

 L V T R H A D V I P V R R R G D S R G S
 361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGACTC CCGTGGTTCC
 GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG

 L L S P R P I S Y L K G S S G G P L L C
 421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTTCT CCGGTGGTCC GCTGCTGTGC
 GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACACG

 P A G H A V G I F R A A V S T R G V A K
 481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT CCACCCGTGG TGTGCTAAA
 GGCCGACCAG TGCACAAACC ATAGAAGGCA CGACGACAAA GGTGGGCACC ACAACGATTT

 A V D F I P V E S L E T T M R S P *
 541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TCGTTCCTCC GTGA
 CGACAACCTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

FIG. 15

M K K K G S V V I V G R I N L S G D T A
1 ATGAAAAAA AAGGATCCGT TGTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT
TACTTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA

Y A Q Q T R G E Q G C Q K T S H T G R D
61 TACGCTCAGC AGACTCGAGG TGAGCAGGGT TGCCAGAAGA CCTCCCACAC CGGTCGTGAC
ATGCGAGTCG TCTGAGCTCC ACTCGTCCCA ACGGTCTTCT GGAGGGTGTG GCCAGCACTG

K N Q V E G E V Q I V S T A T Q T F L A
121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCACCG CTACCCAGAC CTTCTGGCT
TTTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GATGGGTCTG GAAGGACCGA

T S I N G V L W T V Y H G A G T R T I A
181 ACCTCCATCA ACGGTGTTCT GTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT
TGGAGGTAGT TGCCACAAGA CACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA

S P K G P V T Q M Y T N V D K D L V G W
241 TCCCCGAAAG GTCCGGTTAC CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTGTTGGTGG
AGGGGCTTTC CAGGCCAATG GGTCTACATG TGGTTGCAAC TGTTCCTGGA CCAACCAACC

Q A P Q G S R S L T P C T C G S S D L Y
301 CAGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGACCT GCGGTTCCCTC CGACCTGTAC
GTCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG

L V T R H A D V I P V R R R G D S R G S
361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGA CTG CCGTGGTTCC
GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG

L L S P R P I S Y L K G S S G G P L L C
421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTTCCT CCGGTGGTCC GCTGCTGTGC
GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACACG

P A G H A V G I F R A A V S T R G V A K
481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT CCACCCGTGG TGTTGCTAAA
GGCCGACCAG TGCACAACC ATAGAAGGCA CGACGACAAA GGTGGGCACC ACAACGATTT

A V D F I P V E S L E T T M R S P *
541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGCGTTCCCC GTGA
CGACAACCTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

FIG. 16

M K K K G S V V I V G R I N L S G D T A
1 ATGAAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT
TACTTTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA

Y A Q Q T R G E Q G T Q K T S H T G R D
61 TACGCTCAGC AGACTCGAGG TGAGCAGGGT ACCCAGAAGA CCTCCCACAC CGGTCGTGAC
ATGCGAGTCG TCTGAGCTCC ACTCGTCCCA TGGGTCTTCT GGAGGGTGTG GCCAGCACTG

K N Q V E G E V Q I V S T A T Q T F L A
121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCACCG CTACCCAGAC CTTCTGGCT
TTTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GATGGGTCTG GAAGGACCGA

T S I N G V L W T V Y H G A G T R T I A
181 ACCTCCATCA ACGGTGTTCT GTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT
TGGAGGTAGT TGCCACAAGA CACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA

S P K G P V T Q M Y T N V D K D L V G W
241 TCCCCGAAAG GTCCGGTTAC CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTTGGTTGG
AGGGGCTTTC CAGGCCAATG GGTCTACATG TGGTTGCAAC TGTTTCTGGA CCAACCAACC

Q A P Q G S R S L T P C T C G S S D L Y
301 CAGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGACCT GCGGTTCCCTC CGACCTGTAC
GTCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG

L V T R H A D V I P V R R R G D S R G S
361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC TGGGTGACTC CCGTGGTTCC
GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG

L L S P R P I S Y L K G S S G G P L L C
421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTCTT CCGGTGGTCC GCTGCTGTGC
GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACAG

P A G H A V G I F R A A V S T R G V A K
481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT CCACCCGTGG TGTGCTAAA
GGCCGACCAG TGCACAAACC ATAGAAGGCA CGACGACAAA GGTGGGCACC ACAACGATTT

A V D F I P V E S L E T T M R S P *
541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGCGTTCCCC GTGA
CGACAACTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

FIG. 17

M K K K G S V V I V G R I N L S G D T A
 1 ATGAAAAAA AAGGATCCGT TGTTATCGTC GGCCGTATCA ACCTGTCCGG TGACACCGCT
 TACTTTTTTT TTCCTAGGCA ACAATAGCAG CCGGCATAGT TGGACAGGCC ACTGTGGCGA

 Y A Q Q T R G L L G C I I T S L T G R D
 61 TACGCTCAGC AGACTCGAGG TCTGCTGGGT TGCATCATCA CCTCCCTGAC CGGTCGTGAC
 ATGCGAGTCG TCTGAGCTCC AGACGACCCA ACGTAGTAGT GGAGGGACTG GCCAGCACTG

 K N Q V E G E V Q I V S T A A Q T F L A
 121 AAAAACCAGG TTGAAGGTGA AGTTCAGATC GTTTCCACCG CTGCTCAGAC CTTCCTGGCT
 TTTTGGTCC AACTTCCACT TCAAGTCTAG CAAAGGTGGC GACGAGTCTG GAAGGACCGA

 T C I N G V C W T V Y H G A G T R T I A
 181 ACCTGCATCA ACGGTGTTTG CTGGACCGTT TACCACGGTG CTGGTACCCG TACCATCGCT
 TGGACGTAGT TGCCACAAAC GACCTGGCAA ATGGTGCCAC GACCATGGGC ATGGTAGCGA

 S P K G P V I Q M Y T N V D K D L V G W
 241 TCCCCGAAAG GTCCGGTTAT CCAGATGTAC ACCAACGTTG ACAAAGACCT GGTGTTGG
 AGGGGCTTTC CAGGCCAATA GGTCTACATG TGTTTGCAAC TGTTTCTGGA CCAACCAACC

 P A P Q G S R S L T P C T C G S S D L Y
 301 CCGGCTCCGC AGGGTTCCCG TTCCCTGACC CCGTGCACCT GCGGTTCCCTC CGACCTGTAC
 GGCCGAGGCG TCCCAAGGGC AAGGGACTGG GGCACGTGGA CGCCAAGGAG GCTGGACATG

 L V T R H A D V I P V R R R G D S R G S
 361 CTGGTTACCC GTCACGCTGA CGTTATCCCG GTTCGTCGTC GTGGTGACTC CCGTGGTTCC
 GACCAATGGG CAGTGCGACT GCAATAGGGC CAAGCAGCAG CACCACTGAG GGCACCAAGG

 L L S P R P I S Y L K G S S G G P L L C
 421 CTGCTGTCCC CGCGTCCGAT CTCCTACCTG AAAGGTTCTT CCGGTGGTCC GCTGCTGTGC
 GACGACAGGG GCGCAGGCTA GAGGATGGAC TTTCCAAGGA GGCCACCAGG CGACGACACG

 P A G H A V G I F R A A V C T R G V A K
 481 CCGGCTGGTC ACGCTGTTGG TATCTTCCGT GCTGCTGTTT GCACCCGTGG TGTTGCTAAA
 GGCCGACCAG TGCGACAACC ATAGAAGGCA CGACGACAAA CGTGGGCACC ACAACGATTT

 A V D F I P V E S L E T T M R S P *
 541 GCTGTTGACT TCATCCCGGT TGAATCCCTG GAAACCACCA TGCGTTCCCC GTGA
 CGACAACCTGA AGTAGGGCCA ACTTAGGGAC CTTTGGTGGT ACGCAAGGGG CACT

FIG. 18